

Drifting fronds and drifting alleles: the genetic architecture of the estuarine seaweed *Fucus ceranoides* L.

(Algas e genes à deriva: Arquitetura genética da macroalga estuarina *Fucus ceranoides* L.)

Tese de Doutoramento

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In this thesis I investigated the historical and recurrent processes shaping the genetic make-up of *Fucus ceranoides* L, an estuarine furoid seaweed lacking planktonic developmental stages. I've used a range of molecular markers to describe its population genetic structure throughout its entire range (21 populations ranging from Portugal to N Norway) and at more regional spatial

scales (22 consecutive populations in NW Iberia). Specifically, I examined the expected structuring effects of its particular life-history (habitat isolation, limited dispersal), the patterns of population genetic connectivity (via rafting of adults) at large and small spatial scales, the extent of introgression with related species, and its historical biogeography in the Atlantic.



Sampling *F. ceranoides* in Cantabria, Northern Spain

First, I investigated the patterns of genetic exchange between *F. ceranoides* and two marine congeners and assessed its consequences for the species intraspecific phylogeography. I detected the historical introgression of a single *F. vesiculosus* cytoplasm into *F. ceranoides* gene pool, and its extensive geographic spread concurrently with the species' northwards, post-glacial range expansion. This study documented for the first time the role of genetic surfing in producing extensive introgression in a marine organism. I also focused on the genetic imprints of habitat isolation, restricted dispersal and past range dynamics. The molecular data supported the refugial status of Iberia and the post-glacial colonization of previously glaciated/emerged northern latitudes, whereas the strong genetic differentiation of refugial populations implied very limited gene-flow. These data showed that rare effective dispersal via rafting is largely irrelevant for the genetic connectivity of populations, but not range dynamics (habitat tracking), and that regional genetic divergence (refugial areas) or homogeneity (recently colonized areas) depends on the age and demographic history of populations. Finally, I investigated the processes generating and maintaining high levels of regional genetic divergence in NW Iberia. Iberian *F. ceranoides* were subdivided in three

genetic groups displaying a nearly perfect parapatric distribution. The absence of obvious dispersal barriers in this small shoreline sector suggests that the sharp genetic discontinuities correspond to secondary contact zones of formerly vicariant sub-populations, which are retained despite some migration. These data showed that dispersal into vacant (colonization) and saturated (immigration) habitats have very different genetic effects. I conclude that the modern population structure of *F. ceranoides* largely reflects non-equilibrium conditions resulting from historical patterns of estuarine colonization and strong density-blocking effects, rather than contemporary patterns of gene flow.

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